

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 11:28:39 ; Search time 1101 Seconds

(without alignments)
2981.311 Million cell updates/sec

Title: US-10-082-018a-2

perfect score: 1088

Sequence: 1 gcgtaactccctccgtaat.....caccacccaccactaact 1088

Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 1.0

Searched: 6709644 seqs, 1508466879 residues

Total number of hits satisfying chosen parameters: 13419288

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patients NA New: *

1: /SIDS5/ptodata/2/pna/pctm NEW COMB. seq: *
2: /SIDS5/ptodata/2/pna/US06_NEW COMB. seq: *
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11: /SIDS5/ptodata/2/pna/US11_NEW COMB. seq: *
12: /SIDS5/ptodata/2/pna/US60_NEW COMB. seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 589 54.1 1176 8 US-11-039-880-6 Sequence 6, Appli

2 588 54.0 1140 8 US-11-039-880-6 Sequence 4, Appli

3 132.2 12.2 367778 6 US-11-032-841A-1 Sequence 1, Appli

4 109.8 10.1 908 8 US-11-331-032-5574 Sequence 6574, AP

5 109.4 10.1 2300 12 US-60-762-056-35494 Sequence 35494, AP

6 106.8 9.8 810 8 US-11-331-032-6400 Sequence 6400, AP

7 106.8 9.8 1317241 1 PCT-US06-08981-73 Sequence 73, AP

8 102.4 9.4 980 8 US-11-331-032-6399 Sequence 6339, AP

9 102.4 9.4 1835834 1 PCT-US06-08981-72 Sequence 72, AP

10 101 9.3 2540030 1 PCT-US06-08981-69 Sequence 69, AP

11 100.2 9.2 988 8 US-11-331-032-774 Sequence 774, AP

12 100 9.2 1038 8 US-11-360-355-15948 Sequence 15948, AP

13 99.6 9.2 17265 12 US-60-740-736-152 Sequence 152, AP

14 99 9.1 1971884 1 PCT-US06-08981-70 Sequence 70, AP

15 98.6 9.1 899 8 US-11-353-150-24647 Sequence 24647, AP

16 98.6 9.1 1317241 1 PCT-US06-08981-73 Sequence 73, AP

17 98 9.0 2300 12 US-60-762-056-21229 Sequence 21229, AP

18 97.2 8.9 777 8 US-11-331-032-774 Sequence 1035, AP

19 96.8 8.9 1202 8 US-11-360-355-22884 Sequence 22884, AP

20 96.6 8.9 607 8 US-11-331-032-7335 Sequence 1335, AP

21 95.8 8.8 1099 8 US-11-331-032-6603 Sequence 6603, AP

ALIGNMENTS

RESULT 1

US-11-039-880-6

Sequence 6, Application US/11039880

; GENERAL INFORMATION:

; APPLICANT: Lyon, Jeffrey A.

; APPLICANT: Angov, Evelina

; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite

; TITLE OF INVENTION: Protein-142 Vaccine

; FILE REFERENCE: 013/241/SAP

; CURRENT APPLICATION NUMBER: US/11/039, 880

; CURRENT FILING DATE: 2006-01-24

; PRIORITY APPLICATION NUMBER: US/11/057, 531

; PRIORITY FILING DATE: 2002-01-25

; PRIORITY APPLICATION NUMBER: US 60/347, 564

; PRIORITY FILING DATE: 2001-10-26

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Apple Macintosh Microsoft Word 6.0

; SEQ ID NO: 6

; LENGTH: 1176

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE: B. coli expressed P. falciparum

; OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)

; US-11-039-880-6

Query Match

54.1%; Score 589; DB 8; Length 1176;

Best Local Similarity 54.1%; Pred. No. 5; 8e-04;

Matches 819; Conservative 72.7%; 0; Mismatches 245; Indels 63; Gaps 2;

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Sequence 6356, AP

Sequence 6357, AP

Sequence 6358, AP

Sequence 6359, AP

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GenCore version 5.1.7
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On nucleic - nucleic search, using SW model

Run on: April 4, 2006, 11:41:11 ; Search time 1446 Seconds
 (without alignments)
 3004.414 Million cell updates/sec

Title: US-10-082-018a-2
 Perfect score: 1088
 Sequence: 1gcgtaactcttcgtaat.....caccacaccaccaact 1088

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqb, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA_New.*

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15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

RESULT 1
 US-11-144-833-3
 ; Sequence 3, Application US/11144833
 ; Publication No. US20060118932A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LONGACRE-ANDRE, SHIRLEY
 ; APPLICANT: ROTH, CHARLES
 ; APPLICANT: NATO, FARIDABANO
 ; APPLICANT: BARNWILL, JOHN
 ; APPLICANT: MENDIS, KAMINI
 ; TITL OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT
 ; FILE REFERENCE: 0660-0133.QRPT
 ; CURRENT APPLICATION NUMBER: US/11/144-833
 ; PRIORITY NUMBER: 1997-02-14
 ; PRIORITY FILING DATE: 1997-02-14
 ; PRIORITY APPLICATION NUMBER: FR96-01822
 ; PRIORITY FILING DATE: 1996-02-14
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 3
 ; LENGTH: 279
 ; TYPE: DNA
 ; ORGANISM: Plasmodium falciparum
 US-11-144-833-3

Query Match Similarity 25.5%; Score 277.4; DB 14; Length 279;
 Best Local Similarity 99.6%; Pred. No. 1.le-27;
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 787 AACATTTCACACCACTATGCCATAAAAATATGCCACAAATTCTGGATGTTGAGA 846
 1 AACATTTCACACCACTATGCCATAAAAATATGCCACAAATTCTGGATGTTGAGA 60

QY 847 CATTAGATGAAAGAGAGAGAGATGTTAATGTTAATTCACAGAGGTTAA 906
 61 CATTAGATGAAAGAGAGAGATGTTAATGTTAATTCACAGAGGTTAA 120

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	277.4	25.5	279	14 US-11-144-833-3
2	277.4	25.5	342	14 US-11-144-833-6
3	175.4	25.5	291	14 US-11-144-833-1
4	185.0	17.0	330	14 US-11-144-833-9
5	17.0	354	14 US-11-144-833-4	
6	185.0	17.0	354	14 US-11-144-833-4
7	93.0	8.5	1230	6 US-09-925-065A-77681
8	93.0	8.5	1230	9 US-10-301-480-178923
9	93.0	8.5	1230	10 US-10-301-480-1208422
C	10	93.0	8.5	173602 14 US-11-121-086-25
C	11	92.8	49979	8 US-10-995-561-1343
C	12	92.4	979	10 US-10-301-480-595013
C	13	92.4	8.5	979 10 US-10-301-480-595014
C	14	92.4	8.5	979 10 US-10-301-480-595015
C	15	92.4	8.5	979 10 US-10-301-480-1208422
C	16	92.4	8.5	979 10 US-10-301-480-1208423
C	17	92.4	8.5	979 10 US-10-301-480-1208424
C	18	92.4	980	10 US-10-301-480-595016

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 11:34:31 ; Search time 1029 Seconds
(without alignments)
8743.521 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088

Sequence: 1 gcaatcaatctttcccgtaat.....caccacccaccactaact 1088

Scoring table: IDENTITY_NUC

GapOp 10⁻⁶ , GapExt 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

1: /cgn2_6/prodata/1/pubpna/us07_pubcomb.seq: *

2: /cgn2_6/prodata/1/pubpna/us08_pubcomb.seq: *

3: /cgn2_6/prodata/1/pubpna/us09a_pubcomb.seq: *

4: /cgn2_6/prodata/1/pubpna/us09b_pubcomb.seq: *

5: /cgn2_6/prodata/1/pubpna/us10a_pubcomb.seq: *

6: /cgn2_6/prodata/1/pubpna/us10b_pubcomb.seq: *

7: /cgn2_6/prodata/1/pubpna/us10c_pubcomb.seq: *

8: /cgn2_6/prodata/1/pubpna/us10d_pubcomb.seq: *

9: /cgn2_6/prodata/1/pubpna/us10e_pubcomb.seq: *

10: /cgn2_6/prodata/1/pubpna/us11_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

RESULT 1

US-10-082-018-2

Sequence 2, Application US/10022018

Publication No. US20020144299A1

GENERAL INFORMATION:

APPLICANT: CHEN, Li How

ATTORNEY: MRADE, Henry

TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEIC ACID SEQUENCES AND METHODS FOR INCREASING mRNA LEVELS AND PROTEIN EXPRESSIONS IN CELL SYSTEMS

FILE REFERENCE: 107, 637, 121A

CURRENT APPLICATION NUMBER: US/10/082, 018

PRIOR APPLICATION NUMBER: US/09/175, 684

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2

LENGTH: 1088

TYPE: DNA

ORGANISM: preferably, a bacterium, virus, or parasite

US-10-082-018-2

Query Match 100.0%; Score 1088; DB 5; Length 1088;

Best Local Similarity 100.0%; Pred. No. 1, 2e-147; Mismatches 0; Indels 0; Gaps 0;

Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

Sequence 10, Appli

Sequence 11, Appli

Sequence 12, Appli

Sequence 13, Appli

Sequence 14, Appli

Sequence 15, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 18, Appli

Sequence 19, Appli

Sequence 20, Appli

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Sequence 43, Appli

Sequence 44, Appli

Sequence 45, Appli

ALIGNMENTS

Sequence 1, Appli
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Sequence 45, Appli

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 11:09:31 ; Search time 193 Seconds
 (without alignments)
 10020.658 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088

Sequence: 1 gcgttacttcctccgtta.....caccaccaccaact 1088

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq: *
 2: /cgn2_6/ptodata/1/ina/5_COMB.seq: *
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
 5: /cgn2_6/ptodata/1/ina/H_COMB.seq: *
 6: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq: *
 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq: *
 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq: *
 9: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1088	100.0	1088	3 US-09-175-684A-2
2	1074.8	98.8	1175	3 US-09-500-376-7
3	1065	97.9	1842	3 US-09-117-15B-21
4	1065	97.9	1896	3 US-09-117-415B-17
5	1065	97.9	1896	3 US-09-117-415B-19
6	1065	97.9	1950	3 US-09-117-415B-15
7	1065	97.9	1920	3 US-09-269-874A-1
8	1063.4	97.7	1785	3 US-09-117-415B-1
9	623.6	57.3	4838	3 US-09-269-874A-6
10	623.6	57.3	4894	3 US-09-269-874A-9
11	623.6	57.3	4940	3 US-09-269-874A-2
12	609.6	55.0	1142	3 US-09-175-684A-8
13	601	55.2	1065	3 US-09-175-684A-1
14	598.2	55.0	5181	2 US-08-257-073-10
15	597	54.9	1219	3 US-08-195-705-1
16	597	54.9	1219	3 US-09-500-376-1
17	589	54.1	1128	3 US-09-710-000-9
18	588	54.0	1140	3 US-10-057-531A-6
19	306.6	28.2	1235	3 US-09-500-376-6
20	277.4	25.5	279	3 US-09-125-031C-3
21	277.4	25.5	342	3 US-09-125-031C-6
22	185	17.0	291	3 US-09-125-031C-1
23	185	17.0	330	3 US-09-125-031C-9
24	185	17.0	330	3 US-09-125-031C-9

ALIGNMENTS

RESULT 1
 US-09-175-684A-2
 ; Sequence 2, Application US/09175684A
 ; Patent No. 6593463
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Li, How
 ; APPLICANT: Meade, Harry M.
 ; TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEARIC ACID
 ; TITLE OF INVENTION: SEQUENCES AND METHODS FOR INCREASING mRNA LEVELS AND PROTEIN
 ; TITLE OF INVENTION: EXPRESSION IN CELL SYSTEMS
 ; FILE REFERENCE: 10723001
 ; CURRENT APPLICATION NUMBER: US/09/175,684A
 ; CURRENT FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: US 60/085,649
 ; PRIOR FILING DATE: 1997-10-20
 ; PRIOR FILING DATE: 1997-10-20
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1088
 ; TYPE: DNA
 ; ORGANISM: Plasmodium falciparum
 ; FEATURE: CDS
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1083)
 ; US-09-175-684A-2
 ; Query Match 100.0%; Score 1088; DB 3; Length 1088;
 ; Best Local Similarity 100.0%; Pred. No. 6; 8e-13; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 1088; Conservative 0;
 ; Qy 1 GCAGTAACTCTCGTAAATGATACCTCTAAATGAAATGATGAGGT 60
 ; Db 1 GCAGTAACTCTCGTAAATGATACCTCTAAATGAAATGATGAGGT 60
 ; 61 TATATTAAACCTTACAGGTTTAGAGTTAAACAACTTAAAGGATAC 120
 ; 61 TATATTAAACCTTACAGGTTTAGAGTTAAACAACTTAAAGGATAC 120
 ; 121 GTTATGACITTAATGTTATGTTAAGGTATTTAAATCAGGTTAACTGTA 180
 ; 121 GTTATGACITTAATGTTATGTTAAGGTATTTAAATCAGGTTAACTGTA 180
 ; Qy 181 AATTCAAAATGTTAGATGATGATTAATCCATTAAGATTACATCAGTAT 240
 ; Db 181 AATTCAAAATGTTAGATGATGATTAATCCATTAAGATTACATCAGTAT 240

Run on: April 4, 2006, 10:01:54 ; Search time 746 Seconds (without alignments)
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Title: US-10-082-018A-2

Perfect score: 1088

Sequence: 1 gcaatctaactccctccgtaat.....caccaccacccaccaact 1088

Scoring table: IDBNTR_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001ab:*

5: geneseqn2001ba:*

6: geneseqn2002ab:*

7: geneseqn2002ba:*

8: geneseqn2003ab:*

9: geneseqn2003ba:*

10: geneseqn2003ds:*

11: geneseqn2004ab:*

12: geneseqn2004ba:*

13: geneseqn2005ab:*

14: geneseqn2005ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB	ID	Description
1	1088	100.0	1088	10	ABX15263	ABX15263 P. falciparum
2	1088	100.0	1088	11	ADM86680	ADM86680 Plasmodium
3	1088	100.0	1088	14	ADY84057	ADY84057 Malaria m
4	1086.4	99.9	1088	2	AAX56009	AAX56009 Merozoite
5	1086.4	99.9	1088	2	AAX5587	AAX5587 Merozoite
6	1074.8	98.8	1175	14	ADY21419	ADY21419 Baculovir
7	1074.8	98.8	1175	14	ADX85014	ADX85014 Baculovir
8	1074.8	98.8	1175	14	ADZ2138	ADZ2138 Major merozoite
9	1073.2	98.6	1175	10	ADM60350	ADM60350 Baculovir
10	1065	97.9	1131	6	AD47012	AD47012 Plasmodium
11	1065	97.9	1137	6	AD47008	AD47008 Plasmodium
12	1065	97.9	2	AA79758	AA79758 Chimeric	
13	1065	97.9	1950	2	AA79756	AA79756 Chimeric
14	1065	97.9	5282	8	ABO84134	ABO84134 Plasmodium
15	1065	97.9	5917	6	AD46980	AD46980 Plasmodium
16	1063.4	97.7	1896	2	AA79757	AA79757 Chimeric
17	1057.4	97.2	1119	10	ADB2160	ADB2160 Plasmodium
18	1057	97.2	404	2	Aav53563	Aav53563 P-falciparum
19	1046.2	96.2	1116	10	ADB2162	ADB2162 Plasmodium

ALIGNMENTS

Result No.	Score	Query	Match length	DB	ID	Description
1	1088	100.0	1088	10	ABX15263	ABX15263 standard; DNA; 1088 BP.
2	1088	100.0	1088	11	ADM86680	ADM86680 Plasmodium
3	1088	100.0	1088	14	ADY84057	ADY84057 Malaria m
4	1086.4	99.9	1088	2	AAX56009	AAX56009 Merozoite
5	1086.4	99.9	1088	2	AAX5587	AAX5587 Merozoite
6	1074.8	98.8	1175	14	ADY21419	ADY21419 Baculovir
7	1074.8	98.8	1175	14	ADX85014	ADX85014 Baculovir
8	1074.8	98.8	1175	14	ADZ2138	ADZ2138 Major merozoite
9	1073.2	98.6	1175	10	ADM60350	ADM60350 Baculovir
10	1065	97.9	1131	6	AD47012	AD47012 Plasmodium
11	1065	97.9	1137	6	AD47008	AD47008 Plasmodium
12	1065	97.9	2	AA79758	AA79758 Chimeric	
13	1065	97.9	1950	2	AA79756	AA79756 Chimeric
14	1065	97.9	5282	8	ABO84134	ABO84134 Plasmodium
15	1065	97.9	5917	6	AD46980	AD46980 Plasmodium
16	1063.4	97.7	1896	2	AA79757	AA79757 Chimeric
17	1057.4	97.2	1119	10	ADB2160	ADB2160 Plasmodium
18	1057	97.2	404	2	Aav53563	Aav53563 P-falciparum
19	1046.2	96.2	1116	10	ADB2162	ADB2162 Plasmodium

PT Novel modified malaria merozoite surface protein-1 nucleic acid, useful for increasing mRNA levels and expression of the protein in cell culture

